RAW SEQUENCE LISTING   DATE: 09/12/2001
PATENT APPLICATION: US/09/785,738A TIME: 17:11:46

Input Set : A:\198482.1.txt
Output Set: N:\CRF3\09122001\I785738A.raw ENTERED

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 3 <110> APPLICANT: Sauter, Margret M
 4        Lorbiecke, Rene
 6 <120> TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
 7        CONDITIONS
 9 <130> FILE REFERENCE: 2283/201
11 <140> CURRENT APPLICATION NUMBER: 09/785,738A
12 <141> CURRENT FILING DATE: 2001-02-16
14 <150> PRIOR APPLICATION NUMBER: 60/183,572
15 <151> PRIOR FILING DATE: 2000-02-18
17 <160> NUMBER OF SEQ ID NOS: 18
19 <170> SOFTWARE: PatentIn Ver. 2.1
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22 <211> LENGTH: 872
23 <212> TYPE: DNA
24 <213> ORGANISM: Rice
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27 <221> NAME/KEY: CDS
28 <222> LOCATION: (69)..(668)
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34          Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu
35           1               5                  10
37 gca tgg tac atg gat gat agc gaa gag gac cag agg ctt cct cat cac 158
38 Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His
39  15              20                  25                  30
41 cgc gaa ccc aaa gaa ttc att cct gtt gat aag ctt aca gaa cta gga 206
42 Arg Glu Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly
43              35                  40                  45
45 gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac 254
46 Val Ile Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn
47              50                  55                  60
49 ctg aag aga atc cgc gaa gcc aga ggt tac tct tat gtg gac att tgt 302
50 Leu Lys Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys
51              65                  70                  75
53 gat gtg tgc cca gag aag ctg cca aat tat gaa act aag atc aag agt 350
54 Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser
55          80                  85                  90
57 ttc ttt gaa gaa cac ctg cat acc gat gaa gaa ata cgc tat tgt ctt 398
58 Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu
59  95                  100                 105                 110
62 gaa ggg agt gga tac ttt gat gtg aga gac caa aat gat cag tgg att 446
63 Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile
64                  115                 120                 125
66 cgt ata gca ctg aag aaa gga ggc atg att gtt ctg cct gca ggg atg 494
67 Arg Ile Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met
68                  130                 135                 140
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RAW SEQUENCE LISTING   DATE: 09/12/2001
PATENT APPLICATION: US/09/785,738A   TIME: 17:11:46

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70 tac cac cgc ttt acg ttg gac acc gac aac tat atc aag gca atg cga    542
71 Tyr His Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg
72         145             150             155
74 ctg ttt gtt ggc gat cct gtt tgg aca ccc tac aac cgt ccc cat gac    590
75 Leu Phe Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp
76     160             165             170
78 cat ctt cct gca aga aag gag ttt ttg gct aaa ctt ctc aag tca gaa    638
79 His Leu Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu
80 175             180             185             190
82 ggt gaa aat caa gca gtt gaa ggc ttc tga gggttttgtt gggctcctgc      688
83 Gly Glu Asn Gln Ala Val Glu Gly Phe
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W--> 84   195   200
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86 actgcggttc tatattcaac ctgaataaga tgtgctatag caatgtaaat ttagcacagt 748
88 ggctatggtc gccactcacc aacttgaagt gaaagattta atgatttttg ttaattctta 808
90 tgtatcaatc ggcatatagc atttccgaaa tgtgttttca ataaacagga gtcatgaagc 868
92 tgaa                                                             872
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96 <211> LENGTH: 199
97 <212> TYPE: PRT
98 <213> ORGANISM: Rice
100 <400> SEQUENCE: 2
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103 Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His Arg Glu
104             20             25             30
105 Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly Val Ile
106             35             40             45
107 Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn Leu Lys
108         50             55             60
109 Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys Asp Val
110 65             70             75             80
111 Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser Phe Phe
112             85             90             95
113 Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
114             100             105             110
115 Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Ile
116         115             120             125
117 Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
118     130             135             140
119 Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
120 145             150             155             160
121 Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
122             165             170             175
123 Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu Gly Glu
124             180             185             190
125 Asn Gln Ala Val Glu Gly Phe
126         195
130 <210> SEQ ID NO: 3
131 <211> LENGTH: 980
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RAW SEQUENCE LISTING   DATE: 09/12/2001
PATENT APPLICATION: US/09/785,738A   TIME: 17:11:46

Input Set : A:\198482.1.txt
Output Set: N:\CRF3\09122001\I785738A.raw

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133 <213> ORGANISM: Rice
135 <220> FEATURE:
136 <221> NAME/KEY: CDS
137 <222> LOCATION: (139)..(735)
139 <400> SEQUENCE: 3
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142 aggctatccg gaatcgggag ggtttcccaa taggaaagca actcaggact caggagcggc 120
144 gtctgagagg tttcagag atg gag aac cag ttc cag gat ggc aag gag gag      171
145                     Met Glu Asn Gln Phe Gln Asp Gly Lys Glu Glu
146                      1               5                  10
148 gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt      219
149 Val Ile Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
150          15                  20                  25
152 cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca      267
153 Pro His His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
154          30                  35                  40
156 gag tta gga ata tta agc tgg cgc ctg aat gct gat gac tgg gag aat      315
157 Glu Leu Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
158          45                  50                  55
160 gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tct tac atg      363
161 Asp Glu Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
162 60                  65                  70                  75
164 gat att tgt gat gtg tgt cca gaa aag ctg cca aac tat gag gct aag      411
165 Asp Ile Cys Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys
166                      80                  85                  90
168 ctg aaa aat ttc ttt gaa gaa cac ttg cat act gat gaa gag ata cgc      459
169 Leu Lys Asn Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg
170          95                  100                 105
172 tat tgt ctt gag gga agt gga tac ttc gat gtc agg gac caa aat gat      507
173 Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp
174          110                 115                 120
176 cag tgg atc cgt gta gca gtg aag aaa ggg ggc atg att gtt ttg cct      555
177 Gln Trp Ile Arg Val Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro
178          125                 130                 135
180 gcg gga atg tat cac cgc ttc aca ttg gac agt gac aac tac atc aag      603
181 Ala Gly Met Tyr His Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys
182 140                 145                 150                 155
184 gca atg cgg ctc ttt gtg gga gag cct gtc tgg acg ccg tac aac cgt      651
185 Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg
186          160                 165                 170
188 ccc cat gac cat ctg cca gct aga aag gag tat gtc gaa aaa att atc      699
189 Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile
190          175                 180                 185
192 aac agg ggt gga act caa gct gtc gaa gct cgt taa aggcatatca          745
193 Asn Arg Gly Gly Thr Gln Ala Val Glu Ala Arg
194          190                 195
196 agatgtgctt cctagttcgg tgttctgtta cactctacag atactgaata aactgtgcta 805
198 tcagctgttg caatgggctc ctaccgacat cttacatcat ttggcagtat tttgcacaaa 865
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PATENT APPLICATION: US/09/785,738A   TIME: 17:11:46

Input Set : A:\198482.1.txt
Output Set: N:\CRF3\09122001\I785738A.raw

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200 cccgcttaaa atctccctga aaatacgcac gtcaccatgt cagagtgttt atatacaata 925
202 atgacacttc agtccacagt cagcaaggga ctaatgacaa aaaaaaaaaa aaaaa      980
205 <210> SEQ ID NO: 4
206 <211> LENGTH: 198
207 <212> TYPE: PRT
208 <213> ORGANISM: Rice
210 <400> SEQUENCE: 4
211 Met Glu Asn Gln Phe Gln Asp Gly Lys Glu Glu Val Ile Glu Ala Trp
212  1               5                  10                  15
213 Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His Arg Glu
214             20                  25                  30
215 Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser Glu Leu Gly Ile Leu
216         35                  40                  45
217 Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn Asp Glu Asn Leu Lys
218     50                  55                  60
219 Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met Asp Ile Cys Asp Val
220  65                  70                  75                  80
221 Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys Leu Lys Asn Phe Phe
222             85                  90                  95
223 Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
224             100                 105                 110
225 Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Val
226         115                 120                 125
227 Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
228     130                 135                 140
229 Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
230 145                 150                 155                 160
231 Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
232             165                 170                 175
233 Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile Asn Arg Gly Gly Thr
234             180                 185                 190
235 Gln Ala Val Glu Ala Arg
236         195
240 <210> SEQ ID NO: 5
241 <211> LENGTH: 774
242 <212> TYPE: DNA
243 <213> ORGANISM: Tomato
245 <220> FEATURE:
246 <221> NAME/KEY: CDS
247 <222> LOCATION: (1)..(591)
249 <400> SEQUENCE: 5
250 gca cca gat cca aga gag gat gtc ata cag gca tgg tac atg gat gac      48
251 Ala Pro Asp Pro Arg Glu Asp Val Ile Gln Ala Trp Tyr Met Asp Asp
252  1               5                  10                  15
254 aac gat gag gac cag agg ctt cct cat cac cgt gag cca aag gaa ttt      96
255 Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
256             20                  25                  30
258 gtg tct ctt gac aag ctg gct gaa ctt gga gtg ctc agc tgg aga ctt     144
259 Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
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Input Set : A:\198482.1.txt
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260        35              40              45
262 gat gct gac aat tat gag act gat gag gag ttg aag aaa att cgg gaa  192
263 Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
264        50              55              60
266 gat cgt gga tat tca tac att gat ttc tgt gag gtt tgc cct gag aaa  240
267 Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
268 65              70              75              80
270 cta ccg aat tac gag gag aaa atc aag aac ttt ttt gaa gaa cac ctg  288
271 Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
272                85              90              95
274 cac acc gac gag gag atc cgt tac gct gtt gca gga agt ggt tac ttt  336
275 His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
276           100             105             110
278 gat gtc cgc gat gtg aat gag agc tgg att cgc gtc tgg gta aag aaa  384
279 Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
280        115             120             125
282 ggt gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt  432
283 Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
284        130             135             140
286 gat tca agc aac tac att aag gca atg cgt ctc ttt gtt ggt gac cca  480
287 Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
288 145             150             155             160
290 att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa  528
291 Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
292              165             170             175
294 gaa tat gtt gag acg ttt gtc aac gca gat ggc gct ggt cgt gct gtt  576
295 Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val
296           180             185             190
298 aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt  631
299 Asn Ala Ala Ala
300           195
302 aataaatatt accatatggt ggctttgctg ttcttgatgt gtgccttact aagcatgttt 691
304 aatgttgtat tgtggcacta aataaatcac cccctatggg agattgattg tttatatgca 751
306 agtggaattt attatgtgat ttt                                        774
309 <210> SEQ ID NO: 6
310 <211> LENGTH: 196
311 <212> TYPE: PRT
312 <213> ORGANISM: Tomato
314 <400> SEQUENCE: 6
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316 1              5               10              15
317 Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
318           20              25              30
319 Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
320        35              40              45
321 Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
322        50              55              60
323 Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
324 65              70              75              80
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VERIFICATION SUMMARY   DATE: 09/12/2001
PATENT APPLICATION: US/09/785,738A   TIME: 17:11:47

Input Set : A:\198482.1.txt
Output Set: N:\CRF3\09122001\I785738A.raw

L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:400 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:822 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:932 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:934 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17